Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method of analyzing a collection of genetically modified cell strains that are congenic with a parent strain, the method comprising:

(a) receiving images of phenotypes for each of the genetically modified cell strains;

(b) analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) comparing the quantitative representations of the phenotypes ~~with (i) each other, (ii) a qualitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains~~ with a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains, and wherein the cell that is genetically similar or identical has been treated with a drug or a drug candidate.

2. (Original) The method of claim 1, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

3. (Original) The method of claim 2, wherein the deletion mutants each lack a single gene present in the parent strain.

4. (Original) The method of claim 3, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

5. (Original) The method of claim 4, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

6. (Original) The method of claim 5, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae.*

7. (Currently Amended) A method of analyzing a collection of genetically modified cell strains that are congenic with a parent strain, the method comprising: ~~The method of claim 1, further comprising:~~

marking one or more cell features of the genetically modified cell strains so that said features can be highlighted in the images of the phenotypes; ~~and~~

imaging the genetically modified cell strains to produce the images of the phenotypes, wherein the cell features are highlighted in the images of the phenotypes;

receiving images of phenotypes for each of the genetically modified cell strains;

analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

comparing the quantitative representations of the phenotypes with (i) each other, (ii) a quantitative representation of a phenotype of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains,

wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features comprises staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton.

8. (Cancelled)

9. (Original) The method of claim 8, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

10. (Original) The method of claim 1, wherein analyzing the images comprises:

receiving the intensity versus position data from one or markers on the genetically modified cell strains;

quantifying geometrical information about said markers; and

quantifying biological information about said genetically modified cell strains.

11. (Original) The method of claim 10, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

12. (Original) The method of claim 1, wherein comparing the quantitative representations of the phenotypes comprises comparing the quantitative representations of the

phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

13. (Cancelled)

14. (Original) The method of claim 1, further comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

15. (Original) The method of claim 14, further comprising linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

16. (Original) A computer program product comprising a machine readable medium on which is provided program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain, the instructions comprising:

(a) code for receiving images of phenotypes for each of the genetically modified cell strains;

(b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) code for comparing the quantitative representations of the phenotypes ~~with (i) each other, (ii) a qualitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains~~ with a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains, and wherein the cell that is genetically similar or identical has been treated with a drug or a drug candidate.

17. (Original) The computer program product of claim 16, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

18. (Original) The computer program product of claim 17, wherein the deletion mutants each lack a single gene present in the parent strain.

19. (Original) The computer program product of claim 18, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

20. (Original) The computer program product of claim 19, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

21. (Original) The computer program product of claim 20, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae.*

22. (Original) The computer program product of claim 16, further comprising:

code for imaging the genetically modified cell strains to produce the images of the phenotypes, wherein one or more cell features are highlighted by marking in the images of the phenotypes.

23. (Original) The computer program product of claim 22, wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features was accomplished by staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton.

24. (Original) The computer program product of claim 23, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

25. (Original) The computer program product of claim 16, wherein the code for analyzing the images comprises:

code for receiving the intensity versus position data from one or markers on the genetically modified cell strains;

code for quantifying geometrical information about said markers; and

code for quantifying biological information about said genetically modified cell strains.

26. (Original) The computer program product of claim 25, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

27. (Original) The computer program product of claim 16, wherein the code for comparing the quantitative representations of the phenotypes comprises code for comparing the quantitative representations of the phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

28. (Cancelled)

29. (Original) The computer program product of claim 16, further code for comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

30. (Original) The computer program product of claim 29, further comprising code for linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

31. (Original) A computing device comprising a memory device configured to store at least temporarily program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain, the instructions comprising:

(a) code for receiving images of phenotypes for each of the genetically modified cell strains;

(b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) code for comparing the quantitative representations of the phenotypes with ~~(i) each other, (ii) a qualitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains~~ a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains, and wherein the cell that is genetically similar or identical has been treated with a drug or a drug candidate.

32. (New) The method of claim 7, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

33. (New) The method of claim 32, wherein the deletion mutants each lack a single gene present in the parent strain.

34. (New) The method of claim 33, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

35. (New) The method of claim 34, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

36. (New) The method of claim 35, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae.*

37. (New) The method of claim 7, wherein analyzing the images comprises:

receiving the intensity versus position data from one or markers on the genetically modified cell strains;

quantifying geometrical information about said markers; and

quantifying biological information about said genetically modified cell strains.

38. (New) The method of claim 37, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

39. (New) The method of claim 7, wherein comparing the quantitative representations of the phenotypes comprises comparing the quantitative representations of the phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

40. (New) The method of claim 7, further comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

41. (New) The method of claim 40, further comprising linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

42. (New) A computer program product comprising a machine readable medium on which is provided program instructions for analyzing a collection of genetically modified cell strains that are congenic with a parent strain wherein the genetically modified cell strains are yeast strains; wherein one or more cell features of the genetically modified cell strains have been marked so that said features can be highlighted in the images of the phenotype; and wherein said one or more cell features comprises staining the yeast strains with a first stain for the cell wall, a

second stain for the genetic material, and a third stain for the cytoskeleton, the instructions comprising:

(a) code for receiving images of phenotypes for each of the genetically modified cell strains wherein the cell features are highlighted in said images of the phenotypes;

(b) code for analyzing the images with one or more algorithms that provide quantitative representations of the phenotypes; and

(c) code for comparing the quantitative representations of the phenotypes with (i) each other, (ii) a quantitative representation of the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains

43. (New) The computer program product of claim 42, wherein the genetically modified cell strains are deletion mutants having one or more genes deleted from the genome of the parent strain.

44. (New) The computer program product of claim 43, wherein the deletion mutants each lack a single gene present in the parent strain.

45. (New) The computer program product of claim 44, wherein the collection of genetically modified cell strains contains a deletion mutant for each non-essential gene in the parent strain.

46. (New) The computer program product of claim 45, wherein the collection of genetically modified cell strains includes the deletion mutants provided by the *Saccharomyces cerevisiae* Deletion Consortium.

47. (New) The computer program product of claim 46, wherein the collection of genetically modified cell strains further comprises mutant strains having modified, but not deleted, essential genes of *Saccharomyces cerevisiae.*

48. (New) The computer program product of claim 42, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

49. (New) The computer program product of claim 42, wherein the code for analyzing the images comprises:

code for receiving the intensity versus position data from one or markers on the genetically modified cell strains;

code for quantifying geometrical information about said markers; and

code for quantifying biological information about said genetically modified cell strains.

50. (New) The computer program product of claim 49, wherein the quantitative representations of the phenotypes include one or both of the geometrical information and the biological information.

51. (New) The computer program product of claim 42, wherein the code for comparing the quantitative representations of the phenotypes comprises code for comparing the quantitative representations of the phenotypes with each other to cluster the phenotypes and identify common functional traits shared between multiple genetic modifications.

52. (New) The computer program product of claim 42, further code for comprising generating a database including records identifying the phenotypes and the quantitative representations of the phenotypes.

53. (New) The computer program product of claim 52, further comprising code for linking the database with another database containing non-morphological information about the collection of genetically modified cell strains or similar, unmodified parent strains.

54. (New) The method of claim 1, further comprising:

marking one or more cell features of the genetically modified cell strains so that said features can be highlighted in the images of the phenotypes; and

imaging the genetically modified cell strains to produce the images of the phenotypes, wherein the cell features are highlighted in the images of the phenotypes.

55. (New) The method of claim 1, wherein the genetically modified cell strains are yeast strains and wherein marking one or more cell features comprises staining the yeast strains with a first stain for the cell wall, a second stain for the genetic material, and a third stain for the cytoskeleton.

56. (New) The method of claim 55, wherein the first stain is concanavalin A, the second stain is DAPI, and the third stain is rhodamine phalloidin.

REMARKS/ARGUMENTS

Applicants respectfully request reconsideration of the rejections set forth in the Office Action mailed on September 24, 2003. Claims 32-56 have been added. Claim 7 has been rewritten in independent form. The added claims correspond to the originally filed and examined claims but have been modified so to change their dependencies. The title has been amended herein to address the Examiner's concerns. Claims 8, 13 and 28 have been cancelled. Claims 1-7, 9-12, 14-27, and 29-56 are pending. All claims have been rejected.

This amendment is to expedite prosecution and should not be construed as acquiescence in any ground of rejection. Applicants reserve the right to prosecute the originally filed claims, and any other claims supported by the specification, in the future. The comments in the Office action are now addressed in turn.

Rejections under 35 U.S.C. §112, 2nd Paragraph

Claims 1-31 been rejected under 35 U.S.C. §112, second paragraph, as allegedly being indefinite for failing to particularly point out and claim the invention. Applicants respectfully traverse this rejection.

The Office has indicated that the relationship between part (b) of claim 1 with part (c) is unclear. Applicants respectfully maintain that the claim as filed is clear. Specifically, a quantitative representation of a phenotype is compared to a quantitative representation of (i) each other, (ii) the parent strain, or (iii) a quantitative representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains. See, Specification at page 2. Applicants believe that, with the amendments to the claims, the Examiner's concerns have been addressed. Applicants request that it be withdrawn.

Rejections under 35 U.S.C. §102

Claims 1-3, 7, 10-12, 1 4-18, 22, 25-27, and 29-31 have been rejected under 35 U.S.C. §102(b) and (e)(2) as allegedly being anticipated by Kamentsky et al. U.S. Patent No. 5,427,910 ("Kamentsky"). Applicants respectfully traverse this rejection.

As repeatedly indicated by the courts, anticipation requires that all of the elements and limitations of the claim be found within a single prior art reference. There must be no difference between the claimed invention and the disclosure provided by the reference, as viewed by a

person of ordinary skill in the field of the invention. (*Scripps Clinic & Research Fdtn. v. Genentech, Inc.*, 927 F.2d 1565, 1576 [Fed. Cir. 1991]). Furthermore, "[t]o establish *prima facie* obviousness of a claimed invention, all the claim limitations must be taught or suggested by the prior art. (*In re Royka*, 490 F.2d 981, 180 USPQ 580 [CCPA 1974]).

The Office has cited Kamentsky as describing the imaging of cells and more particularly, chromosomes. The Office contends that these images are phenotypes as they are visual representations of the cells being imaged. The Office further argues that the various algorithms are then applied to the signals to correct for background and generate distance parameters. The "phenotype" is then compared to genetically similar ones as to chromosome number.

Applicants respectfully maintain that the cited art does not teach or suggest the invention, as claimed herein. Specifically, Kamentsky does not teach or suggest the comparison of a quantitative representation of a phenotype with a representation of a phenotype of a cell that is genetically similar or identical to one or more of the cell strains *and* has been treated with a drug or drug candidate as in Claim 1. Nor does Kamentsky teach or suggest marking one or cell features (and more particularly, the cell wall, genetic material, and/or cytoskeleton of one or more yeast strains) so that the features can be highlighted in the images of the phenotype as in Claim 7. Rather, Applicants note that Kamentsky indicates at column 2, line 65 to column 3, line 7, that only two aspects of fluorescence emanating from marked cells can be determined; namely, amount of fluorescence from each "spot" and the number of "spots". The cited art simply does not teach or suggest the invention as claimed herein.

Applicants request that the rejection be withdrawn.

Conclusion

The Applicants respectfully maintain that all pending claims are in condition for allowance. Therefore, the Applicants respectfully request a Notice of Allowance for this Application from the Examiner. Should any unresolved issues remain, the Examiner is encouraged to contact the undersigned at the telephone number provided below.

Respectfully submitted,
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